APPLYING METABOLIC MODELS FOR CONTROL IN ORDER TO ENHANCE ALGAL GROWTH AND LIPID PRODUCTION

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Key Words: *C. vulgaris*, Metabolic models, Control, Fatty acid methyl ester (FAME)

A number of metabolic models have been developed in different algae species in the past five years. In this study, a metabolic model of *C. vulgaris* was applied for controlling algal growth and lipid production. This method optimized nutrient supply by characterizing algal metabolic pathways under different conditions. The approach was validated for autotrophic growth under nitrogen replete condition, in which nitrate requirement was lowered while retaining robust algal growth. Furthermore, this approach was also applied for nitrogen limited environments. Previous studies have found *C. vulgaris* can accumulate high lipid content in biomass, which can be hydrotreated to biodiesel, while decreasing algal growth under nitrogen limitation [1]. Our method optimized the nitrate supply to sustain algal growth while still producing fatty acids efficiently under nitrogen limited conditions. Compared with *C. vulgaris* cultures with complete nitrogen withdrawal, fatty acid methyl esters (FAME) increased substantially. This metabolic model-based approach will have applicability for optimizing nutrient inputs and biomanufacturing across a wide spectrum of organisms ranging from prokaryotes to eukaryotes used to produce a variety of biotechnology products in coming decades.

References

[1] M.T. Guarnieri, A. Nag, S.L. Smolinski, A. Darzins, M. Seibert, P.T. Pienkos, Examination of triacylglycerol biosynthetic pathways via de novo transcriptomic and proteomic analyses in an unsequenced microalga, PLoS One, 6 (2011) e25851.